

Kaufman

1646

#5
MB
04/24/98

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/906,713

DATE: 04/10/98
TIME: 14:35:18

INPUT SET: S24888.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Lok, Si
6 Adams, Robyn L.
7 Jelmsberg, Anna C.
8 Whitmore, Theodore E.
9 Farrah, Theresa M.
10
11 (ii) TITLE OF THE INVENTION: MAMMALIAN ZCYTOR11
12
13
14 (iii) NUMBER OF SEQUENCES: 6
15
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Zymogenetics
18 (B) STREET: 1201 Eastlake Ave East
19 (C) CITY: Seattle
20 (D) STATE: WA
21 (E) COUNTRY: USA
22 (F) ZIP: 98102
23
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Diskette
26 (B) COMPUTER: IBM Compatible
27 (C) OPERATING SYSTEM: DOS
28 (D) SOFTWARE: FastSEQ for Windows Version 2.0
29
30 (vi) CURRENT APPLICATION DATA:
31 (A) APPLICATION NUMBER:
32 (B) FILING DATE:
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER:
37 (B) FILING DATE:
38
39
40
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: Lunn, Paul G
43 (B) REGISTRATION NUMBER: 32,743
44 (C) REFERENCE/DOCKET NUMBER: 97-52
45
46 (ix) TELECOMMUNICATION INFORMATION:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/906,713

 DATE: 04/10/98
 TIME: 14:35:19

INPUT SET: S24888.raw

47 (A) TELEPHONE: 206-442-6627
 48 (B) TELEFAX: 206-442-6678
 49 (C) TELEX:

50
 51
 52 (2) INFORMATION FOR SEQ ID NO:1:
 53

54 (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 2831 base pairs
 56 (B) TYPE: nucleic acid
 57 (C) STRANDEDNESS: single
 58 (D) TOPOLOGY: linear
 59

60 (ii) MOLECULE TYPE: cDNA

61 (ix) FEATURE:

62
 63 (A) NAME/KEY: Coding Sequence
 64 (B) LOCATION: 34...1755
 65 (D) OTHER INFORMATION:
 66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 68

| | | |
|----|--|-----|
| 69 | TAGAGGCCAA GGGAGGGCTC TGTGCCAGCC CCG ATG AGG ACG CTG CTG ACC ATC | 54 |
| 70 | Met Arg Thr Leu Leu Thr Ile | |
| 71 | 1 5 | |
| 72 | | |
| 73 | TTG ACT GTG GGA TCC CTG GCT GCT CAC GCC CCT GAG GAC CCC TCG GAT | 102 |
| 74 | Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp | |
| 75 | 10 15 20 | |
| 76 | | |
| 77 | CTG CTC CAG CAC GTG AAA TTC CAG TCC AGC AAC TTT GAA AAC ATC CTG | 150 |
| 78 | Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu | |
| 79 | 25 30 35 | |
| 80 | | |
| 81 | ACG TGG GAC AGC GGG CCA GAG GGC ACC CCA GAC ACG GTC TAC AGC ATC | 198 |
| 82 | Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile | |
| 83 | 40 45 50 55 | |
| 84 | | |
| 85 | GAG TAT AAG ACG TAC GGA GAG AGG GAC TGG GTG GCA AAG AAG GGC TGT | 246 |
| 86 | Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys | |
| 87 | 60 65 70 | |
| 88 | | |
| 89 | CAG CGG ATC ACC CGG AAG TCC TGC AAC CTG ACG GTG GAG ACG GGC AAC | 294 |
| 90 | Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn | |
| 91 | 75 80 85 | |
| 92 | | |
| 93 | CTC ACG GAG CTC TAC TAT GCC AGG GTC ACC GCT GTC AGT GCG GGA GGC | 342 |
| 94 | Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly | |
| 95 | 90 95 100 | |
| 96 | | |
| 97 | CGG TCA GCC ACC AAG ATG ACT GAC AGG TTC AGC TCT CTG CAG CAC ACT | 390 |
| 98 | Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr | |
| 99 | 105 110 115 | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|
| 100 | | | | | | | | | | | | | | | | | | |
| 101 | ACC | CTC | AAG | CCA | CCT | GAT | GTG | ACC | TGT | ATC | TCC | AAA | GTG | AGA | TCG | ATT | | 438 |
| 102 | Thr | Leu | Lys | Pro | Pro | Asp | Val | Thr | Cys | Ile | Ser | Lys | Val | Arg | Ser | Ile | | |
| 103 | 120 | | | | | 125 | | | | | 130 | | | | | 135 | | |
| 104 | | | | | | | | | | | | | | | | | | |
| 105 | CAG | ATG | ATT | GTT | CAT | CCT | ACC | CCC | ACG | CCA | ATC | CGT | GCA | GGC | GAT | GGC | | 486 |
| 106 | Gln | Met | Ile | Val | His | Pro | Thr | Pro | Thr | Pro | Ile | Arg | Ala | Gly | Asp | Gly | | |
| 107 | | | | | 140 | | | | | | 145 | | | | 150 | | | |
| 108 | | | | | | | | | | | | | | | | | | |
| 109 | CAC | CGG | CTA | ACC | CTG | GAA | GAC | ATC | TTC | CAT | GAC | CTG | TTC | TAC | CAC | TTA | | 534 |
| 110 | His | Arg | Leu | Thr | Leu | Glu | Asp | Ile | Phe | His | Asp | Leu | Phe | Tyr | His | Leu | | |
| 111 | | | | 155 | | | | | 160 | | | | | 165 | | | | |
| 112 | | | | | | | | | | | | | | | | | | |
| 113 | GAG | CTC | CAG | GTC | AAC | CGC | ACC | TAC | CAA | ATG | CAC | CTT | GGA | GGG | AAG | CAG | | 582 |
| 114 | Glu | Leu | Gln | Val | Asn | Arg | Thr | Tyr | Gln | Met | His | Leu | Gly | Gly | Lys | Gln | | |
| 115 | | | 170 | | | | | 175 | | | | | 180 | | | | | |
| 116 | | | | | | | | | | | | | | | | | | |
| 117 | AGA | GAA | TAT | GAG | TTC | TTC | GGC | CTG | ACC | CCT | GAC | ACA | GAG | TTC | CTT | GGC | | 630 |
| 118 | Arg | Glu | Tyr | Glu | Phe | Phe | Gly | Leu | Thr | Pro | Asp | Thr | Glu | Phe | Leu | Gly | | |
| 119 | | 185 | | | | | 190 | | | | | 195 | | | | | | |
| 120 | | | | | | | | | | | | | | | | | | |
| 121 | ACC | ATC | ATG | ATT | TGC | GTT | CCC | ACC | TGG | GCC | AAG | GAG | AGT | GCC | CCC | TAC | | 678 |
| 122 | Thr | Ile | Met | Ile | Cys | Val | Pro | Thr | Trp | Ala | Lys | Glu | Ser | Ala | Pro | Tyr | | |
| 123 | 200 | | | | | 205 | | | | | 210 | | | | | 215 | | |
| 124 | | | | | | | | | | | | | | | | | | |
| 125 | ATG | TGC | CGA | GTG | AAG | ACA | CTG | CCA | GAC | CGG | ACA | TGG | ACC | TAC | TCC | TTC | | 726 |
| 126 | Met | Cys | Arg | Val | Lys | Thr | Leu | Pro | Asp | Arg | Thr | Trp | Thr | Tyr | Ser | Phe | | |
| 127 | | | | | 220 | | | | | 225 | | | | | 230 | | | |
| 128 | | | | | | | | | | | | | | | | | | |
| 129 | TCC | GGA | GCC | TTC | CTG | TTC | TCC | ATG | GGC | TTC | CTC | GTC | GCA | GTA | CTC | TGC | | 774 |
| 130 | Ser | Gly | Ala | Phe | Leu | Phe | Ser | Met | Gly | Phe | Leu | Val | Ala | Val | Leu | Cys | | |
| 131 | | | | 235 | | | | | 240 | | | | | 245 | | | | |
| 132 | | | | | | | | | | | | | | | | | | |
| 133 | | | | | | | | | | | | | | | | | | |
| 134 | TAC | CTG | AGC | TAC | AGA | TAT | GTC | ACC | AAG | CCG | CCT | GCA | CCT | CCC | AAC | TCC | | 822 |
| 135 | Tyr | Leu | Ser | Tyr | Arg | Tyr | Val | Thr | Lys | Pro | Pro | Ala | Pro | Pro | Asn | Ser | | |
| 136 | | | 250 | | | | | 255 | | | | | 260 | | | | | |
| 137 | | | | | | | | | | | | | | | | | | |
| 138 | CTG | AAC | GTC | CAG | CGA | GTC | CTG | ACT | T | | | | | | | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| 153 | | | | | | | | | | | | | | | | | | |
| 154 | GGG | CAG | CCA | GAC | ATC | TCC | ATC | CTC | CAG | CCC | TCC | AAC | GTG | CCA | CCT | CCC | | 1062 |
| 155 | Gly | Gln | Pro | Asp | Ile | Ser | Ile | Leu | Gln | Pro | Ser | Asn | Val | Pro | Pro | Pro | | |
| 156 | | | 330 | | | | | 335 | | | | | 340 | | | | | |
| 157 | | | | | | | | | | | | | | | | | | |
| 158 | CAG | ATC | CTC | TCC | CCA | CTG | TCC | TAT | GCC | CCA | AAC | GCT | GCC | CCT | GAG | GTC | | 1110 |
| 159 | Gln | Ile | Leu | Ser | Pro | Leu | Ser | Tyr | Ala | Pro | Asn | Ala | Ala | Pro | Glu | Val | | |
| 160 | | 345 | | | | | 350 | | | | | 355 | | | | | | |
| 161 | | | | | | | | | | | | | | | | | | |
| 162 | GGG | CCC | CCA | TCC | TAT | GCA | CCT | CAG | GTG | ACC | CCC | GAA | GCT | CAA | TTC | CCA | | 1158 |
| 163 | Gly | Pro | Pro | Ser | Tyr | Ala | Pro | Gln | Val | Thr | Pro | Glu | Ala | Gln | Phe | Pro | | |
| 164 | 360 | | | | | 365 | | | | | 370 | | | | | 375 | | |
| 165 | | | | | | | | | | | | | | | | | | |
| 166 | TTC | TAC | GCC | CCA | CAG | GCC | ATC | TCT | AAG | GTC | CAG | CCT | TCC | TCC | TAT | GCC | | 1206 |
| 167 | Phe | Tyr | Ala | Pro | Gln | Ala | Ile | Ser | Lys | Val | Gln | Pro | Ser | Ser | Tyr | Ala | | |
| 168 | | | | | 380 | | | | | 385 | | | | | 390 | | | |
| 169 | | | | | | | | | | | | | | | | | | |
| 170 | CCT | CAA | GCC | ACT | CCG | GAC | AGC | TGG | CCT | CCC | TCC | TAT | GGG | GTA | TGC | ATG | | 1254 |
| 171 | Pro | Gln | Ala | Thr | Pro | Asp | Ser | Trp | Pro | Pro | Ser | Tyr | Gly | Val | Cys | Met | | |
| 172 | | | | 395 | | | | | 400 | | | | | 405 | | | | |
| 173 | | | | | | | | | | | | | | | | | | |
| 174 | GAA | GGT | TCT | GGC | AAA | GAC | TCC | CCC | ACT | GGG | ACA | CTT | TCT | AGT | CCT | AAA | | 1302 |
| 175 | Glu | Gly | Ser | Gly | Lys | Asp | Ser | Pro | Thr | Gly | Thr | Leu | Ser | Ser | Pro | Lys | | |
| 176 | | | 410 | | | | | 415 | | | | | 420 | | | | | |
| 177 | | | | | | | | | | | | | | | | | | |
| 178 | | | | | | | | | | | | | | | | | | |
| 179 | CAC | CTT | AGG | CCT | AAA | GGT | CAG | CTT | CAG | AAA | GAG | CCA | CCA | GCT | GGA | AGC | | 1350 |
| 180 | His | Leu | Arg | Pro | Lys | Gly | Gln | Leu | Gln | Lys | Glu | Pro | Pro | Ala | Gly | Ser | | |
| 181 | | 425 | | | | | 430 | | | | | 435 | | | | | | |
| 182 | | | | | | | | | | | | | | | | | | |
| 183 | TGC | ATG | TTA | GGT | GGC | CTT | TCT | CTG | CAG | GAG | GTG | ACC | TCC | TTG | GCT | ATG | | 1398 |
| 184 | Cys | Met | Leu | Gly | Gly | Leu | Ser | Leu | Gln | Glu | Val | Thr | Ser | Leu | Ala | Met | | |
| 185 | 440 | | | | | 445 | | | | | 450 | | | | | 455 | | |
| 186 | | | | | | | | | | | | | | | | | | |
| 187 | GAG | GAA | TCC | CAA | GAA | GCA | AAA | TCA | TTG | CAC | CAG | CCC | CTG | GGG | ATT | TGC | | 1446 |
| 188 | Glu | Glu | Ser | Gln | Glu | Ala | Lys | Ser | Leu | His | Gln | Pro | Leu | Gly | Ile | Cys | | |
| 189 | | | | | 460 | | | | | 465 | | | | | 470 | | | |
| 190 | | | | | | | | | | | | | | | | | | |
| 191 | ACA | GAC | AGA | ACA | TCT | GAC | CCA | AAT | GTG | CTA | CAC | AGT | GGG | GAG | | | | |

RAW SEQUENCE LISTING PATENT APPLICATION US/08/906,713

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206
207   CTT GTG TGT CCC AAG GAT GAA GCC AAG AGC CCA GCC CCT GAG ACC TCA      1686
208   Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
209                   540                               545                   550
210
211   GAC CTG GAG CAG CCC ACA GAA CTG GAT TCT CTT TTC AGA GGC CTG GCC      1734
212   Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
213                   555                               560                   565
214
215   CTG ACT GTG CAG TGG GAG TCC TGAGGGGAAT GGGAAAGGCT TGGTGCTTCC TCCC      1789
216   Leu Thr Val Gln Trp Glu Ser
217                   570
218
219   TGTCCCTACC CAGTGTCAACA TCCTTGGCTG TCAATCCCAT GCCTGCCCCAT GCCACACACT      1849
220   CTGCGATCTG GCCTCAGACG GGTGCCCTTG AGAGAAGCAG AGGGAGTGGC ATGCAGGGCC      1909
221   CCTGCCATGG GTGCGCTCCT CACCGGAACA AAGCAGCATG ATAAGGACTG CAGCGGGGGA      1969
222   GCTCTGGGGA GCAGCTTGTG TAGACAAGCG CGTGCTCGCT GAGCCCTGCA AGGCAGAAAT      2029
223   GACAGTGCAA GGAGGAAATG CAGGGAAACT CCCGAGGTCC AGAGCCCCAC CTCCTAACAC      2089
224   CATGGATTCA AAGTGCTCAG GGAATTTGCC TCTCCTTGCC CCATTCCTGG CCAGTTTCAC      2149
225   AATCTAGCTC GACAGAGCAT GAGGCCCTG CCTCTTCTGT CATGTGTTCAA AGGTGGGAAG      2209
226   AGAGCCTGGA AAAGAACCAG GCCTGGAAAA GAACCAGAAG GAGGCTGGGC AGAACCAGAA      2269
227   CAACCTGCAC TTCTGCCAAG GCCAGGGCCA GCAGGACGGC AGGACTCTAG GGAGGGGTGT      2329
228   GGCCTGCAGC TCATTCCCAG CCAGGGCAAC TGCCTGACGT TGCACGATTT CAGCTTCATT      2389
229   CCTCTGATAG AACAAAGCGA AATGCAGGTC CACCAGGGAG GGAGACACAC AAGCCTTTTC      2449
230   TGCAGGCAGG AGTTTCAGAC CCTATCCTGA GAATGGGGTT TGAAAGGAAG GTGAGGGCTG      2509
231   TGGCCCCTGG ACGGGTACAA TAACACACTG TACTGATGTC ACAACTTTGC AAGCTCTGCC      2569
232   TTGGGTTTCA CCCATCTGGG CTCAAATTCC AGCCTCACCA CTCACAAGCT GTGTGACTTC      2629
233   AAACAAATGA AATCAGTGCC CAGAACCTCG GTTTCCTCAT CTGTAATGTG GGGATCATAA      2689
234   CACCTACCTC ATGGAGTTGT GGTGAAGATG AAATGAAGTC ATGTCTTTAA AGTGCTTAAT      2749
235   AGTGCCTGGT ACATGGGCAG TGCCCAATAA ACGGTAGCTA TTTAAAAAAA AAAAAAAAAA      2809
236   AAAAAAATAG CGGCCGCCTC GA
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```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 574 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

251   Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
252       1             5             10             15
253   Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
254               20             25             30
255   Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
256           35             40             45
257   Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
258       50             55             60

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/906,713

DATE: 04/10/98
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Line

Error

Original Text